



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 5, 2026 – 04:30 PM EDT

PDB ID : 7KEM / pdb_00007kem
Title : Crystallographic structure of L,D-transpeptidase 2 from Mycobacterium tuberculosis
Authors : Libreros, G.A.; Dias, M.V.B.
Deposited on : 2020-10-11
Resolution : 1.77 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

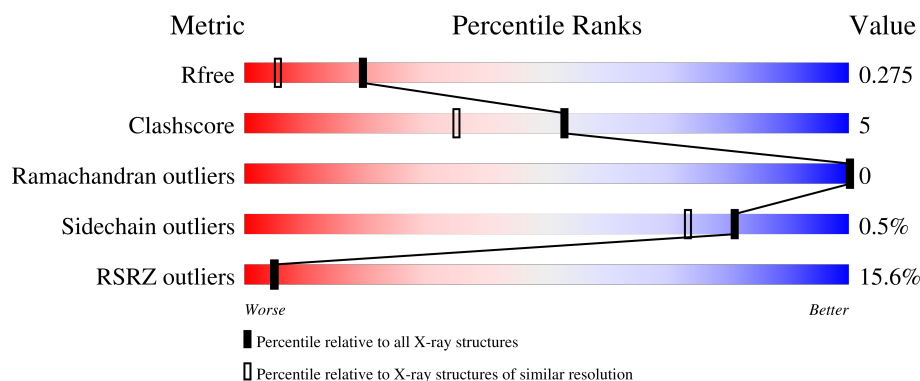
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.77 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1365 (1.78-1.78)
Clashscore	190562	1395 (1.78-1.78)
Ramachandran outliers	187476	1382 (1.78-1.78)
Sidechain outliers	187428	1382 (1.78-1.78)
RSRZ outliers	180081	1365 (1.78-1.78)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	408	
1	B	408	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	DGL	A	505[B]	-	X	-	-

2 Entry composition [i](#)

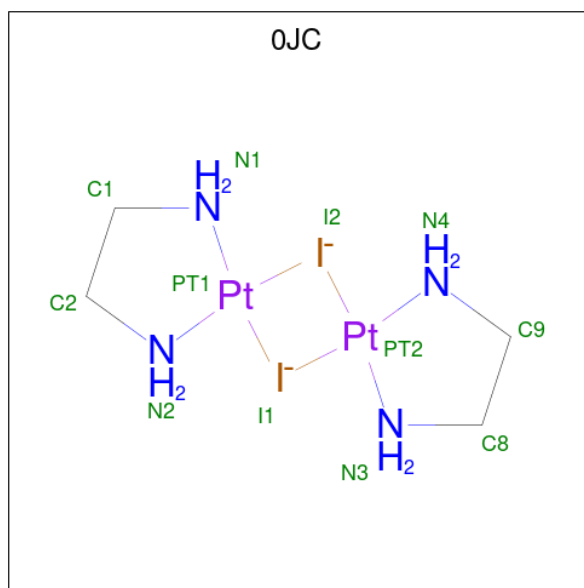
There are 5 unique types of molecules in this entry. The entry contains 4182 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called L,D-transpeptidase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	258	Total	C	N	O	S	0	3	0
			2008	1266	349	385	8			
1	B	269	Total	C	N	O	S	0	2	0
			2063	1301	357	398	7			

- Molecule 2 is Di-mu-iodobis(ethylenediamine)diplatinum(II) (CCD ID: 0JC) (formula: $\text{C}_4\text{H}_{16}\text{I}_2\text{N}_4\text{Pt}_2$).



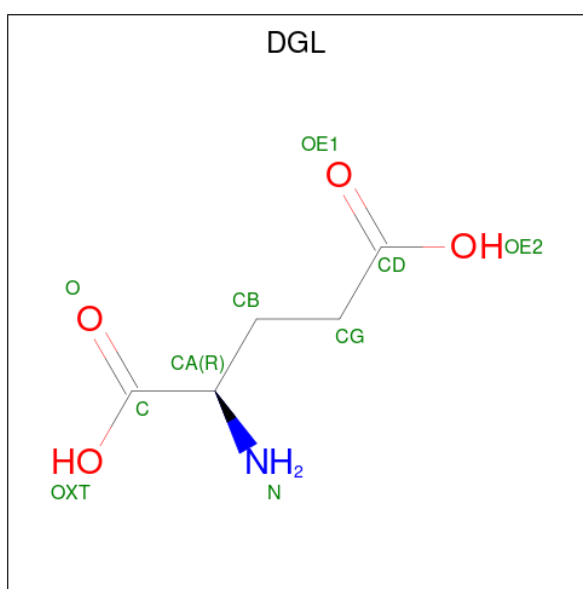
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	I	N	Pt	6	0
			6	2	1	2	1		
2	A	1	Total	C	I	N	Pt	12	1
			12	4	2	4	2		
2	A	1	Total	C	I	N	Pt	6	0
			6	2	1	2	1		
2	A	1	Total	C	I	N	Pt	12	1
			12	4	2	4	2		

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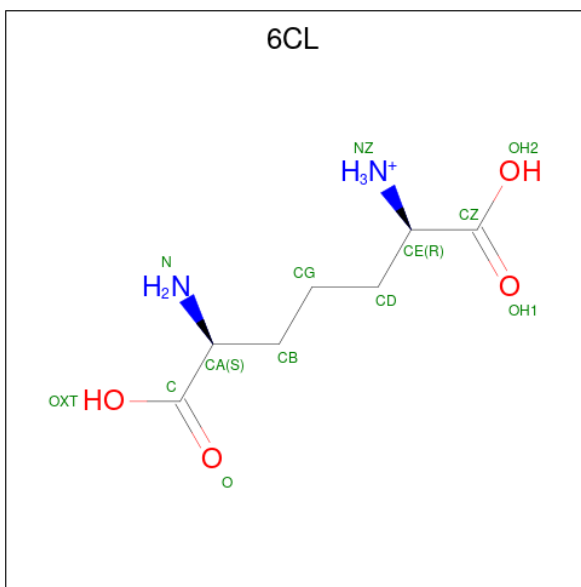
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total 6	C 2	I 1	N 2	Pt 1	6	0
2	B	1	Total 6	C 2	I 1	N 2	Pt 1	6	0
2	B	1	Total 12	C 4	I 2	N 4	Pt 2	12	1
2	B	1	Total 6	C 2	I 1	N 2	Pt 1	6	0

- Molecule 3 is D-GLUTAMIC ACID (CCD ID: DGL) (formula: $C_5H_9NO_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	18	1
			18	10	2	6		

- Molecule 4 is 6-CARBOXYLYSINE (CCD ID: 6CL) (formula: $\text{C}_7\text{H}_{15}\text{N}_2\text{O}_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	N	O	26	1
			26	14	4	8		

- Molecule 5 is PLATINUM (II) ION (CCD ID: PT) (formula: Pt).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Pt	1	0
			1	1		

4 Data and refinement statistics

Property	Value	Source
Space group	I 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	117.53Å 121.05Å 122.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.66 – 1.77 49.66 – 1.77	Depositor EDS
% Data completeness (in resolution range)	99.7 (49.66-1.77) 99.7 (49.66-1.77)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.33 (at 1.77Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.261 , 0.275 0.260 , 0.275	Depositor DCC
R_{free} test set	4222 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	22.7	Xtriage
Anisotropy	0.527	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 18.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.087 for -h,-l,-k 0.010 for l,-k,h 0.013 for -k,-h,-l 0.006 for k,-l,-h 0.006 for -l,h,-k	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4182	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.26% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: DGL, OJC, 6CL, PT

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.60	0/2067	0.99	0/2827
1	B	0.61	0/2125	1.00	1/2905 (0.0%)
All	All	0.60	0/4192	0.99	1/5732 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	122	ARG	CB-CA-C	5.95	121.39	110.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2008	0	1910	14	0
1	B	2063	0	1950	26	0
2	A	36	0	24	0	0
2	B	30	0	20	0	0
3	A	18	0	14	0	0
4	B	26	0	24	0	0
5	B	1	0	0	0	0
All	All	4182	0	3942	40	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

All (40) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:128:ALA:HB2	1:B:156:VAL:HG13	1.26	1.15
1:B:153:MET:HE3	1:B:154:PRO:HD2	1.43	0.99
1:B:289:ASN:HD21	1:B:380:THR:H	1.19	0.89
1:B:291:ILE:H	1:B:395:ASN:HD21	1.20	0.87
1:A:289:ASN:HD21	1:A:380:THR:H	1.21	0.86
1:B:128:ALA:HB2	1:B:156:VAL:CG1	2.05	0.86
1:A:291:ILE:H	1:A:395:ASN:HD21	1.21	0.86
1:B:128:ALA:CB	1:B:156:VAL:HG13	2.08	0.83
1:B:156:VAL:HG12	1:B:243:VAL:HG11	1.67	0.75
1:A:181:ARG:HH21	1:A:205:ASN:HD22	1.36	0.73
1:B:150:HIS:HD2	1:B:151:LEU:HG	1.55	0.70
1:A:224:VAL:HB	1:A:245:THR:HG22	1.82	0.61
1:B:153:MET:HE1	1:B:241:ASP:HB3	1.85	0.58
1:A:181:ARG:HH21	1:A:205:ASN:ND2	2.02	0.58
1:B:131:LEU:O	1:B:132:GLY:C	2.50	0.55
1:B:224:VAL:HB	1:B:245:THR:HG22	1.88	0.55
1:B:297:ARG:HH11	1:B:297:ARG:HG3	1.76	0.50
1:B:297:ARG:HG3	1:B:297:ARG:NH1	2.26	0.50
1:B:339:PRO:HG3	1:B:359:PRO:HG3	1.93	0.50
1:B:156:VAL:CG1	1:B:243:VAL:CG1	2.93	0.47
1:B:156:VAL:CG1	1:B:243:VAL:HG11	2.40	0.47
1:A:291:ILE:N	1:A:395:ASN:HD21	2.02	0.47
1:A:361:ASN:HD22	1:A:361:ASN:HA	1.63	0.46
1:B:156:VAL:HG11	1:B:243:VAL:HG12	1.99	0.44
1:B:291:ILE:N	1:B:395:ASN:HD21	2.01	0.44
1:A:339:PRO:HG3	1:A:359:PRO:HG3	2.00	0.44
1:B:213:GLU:HA	1:B:398:TRP:CE3	2.53	0.43
1:A:179:ALA:HB3	1:A:234:GLY:HA3	2.01	0.43
1:A:213:GLU:HA	1:A:398:TRP:CE3	2.54	0.42
1:A:156:VAL:HG12	1:A:243:VAL:HG11	2.02	0.42
1:A:387:GLY:HA3	1:A:396:ILE:HG13	2.02	0.42
1:B:291:ILE:H	1:B:395:ASN:ND2	2.02	0.42
1:A:200:PHE:HA	1:A:209:ARG:O	2.21	0.41
1:B:402:ARG:HE	1:B:402:ARG:HB3	1.58	0.41
1:B:361:ASN:HD22	1:B:361:ASN:HA	1.63	0.41
1:B:303:MET:HE2	1:B:322:VAL:HG11	2.03	0.41
1:A:289:ASN:HD21	1:A:380:THR:N	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:167:GLY:HA3	1:B:374:ILE:HD11	2.04	0.40
1:B:150:HIS:CD2	1:B:151:LEU:HG	2.45	0.40
1:B:157:MET:HE3	1:B:173:ARG:HH12	1.86	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	259/408 (64%)	253 (98%)	6 (2%)	0	100	100
1	B	267/408 (65%)	261 (98%)	6 (2%)	0	100	100
All	All	526/816 (64%)	514 (98%)	12 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	215/320 (67%)	215 (100%)	0	100	100
1	B	218/320 (68%)	216 (99%)	2 (1%)	70	59
All	All	433/640 (68%)	431 (100%)	2 (0%)	81	73

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	157	MET
1	B	189	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	205	ASN
1	A	289	ASN
1	A	361	ASN
1	A	379	ASN
1	A	395	ASN
1	B	150	HIS
1	B	289	ASN
1	B	361	ASN
1	B	379	ASN
1	B	395	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 1 is monoatomic - leaving 15 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	6CL	B	501[A]	3	10,12,12	1.72	2 (20%)	9,15,15	2.42	4 (44%)
2	0JC	B	504	-	3,6,14	0.59	0	2,7,22	0.60	0
2	0JC	B	505[A]	-	3,6,14	0.44	0	2,7,22	0.61	0
4	6CL	B	501[B]	3	10,12,12	1.67	2 (20%)	9,15,15	2.34	2 (22%)
2	0JC	A	503	-	3,6,14	0.53	0	2,7,22	0.21	0
2	0JC	A	504[A]	-	3,6,14	0.49	0	2,7,22	0.48	0
2	0JC	B	505[B]	1	3,6,14	0.42	0	2,7,22	2.57	1 (50%)
3	DGL	A	505[A]	4	6,8,9	1.53	1 (16%)	6,9,11	2.40	4 (66%)
2	0JC	A	504[B]	-	3,6,14	0.48	0	2,7,22	0.60	0
2	0JC	A	501	1	3,6,14	0.62	0	2,7,22	0.44	0
3	DGL	A	505[B]	4	6,8,9	1.14	1 (16%)	6,9,11	1.58	2 (33%)
2	0JC	B	503	1	3,6,14	0.42	0	2,7,22	0.58	0
2	0JC	A	502[A]	-	3,6,14	0.65	0	2,7,22	0.77	0
2	0JC	B	506	1	3,6,14	0.51	0	2,7,22	0.90	0
2	0JC	A	502[B]	1	3,6,14	0.26	0	2,7,22	0.41	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	6CL	B	501[A]	3	-	9/14/14/14	-
2	0JC	B	504	-	-	-	0/1/1/3
2	0JC	B	505[A]	-	-	-	0/1/1/3
4	6CL	B	501[B]	3	-	9/14/14/14	-
2	0JC	A	503	-	-	-	0/1/1/3
2	0JC	A	504[A]	-	-	-	0/1/1/3
2	0JC	B	505[B]	1	-	-	0/1/1/3
3	DGL	A	505[A]	4	-	1/8/8/9	-
2	0JC	A	504[B]	-	-	-	0/1/1/3
2	0JC	A	501	1	-	-	0/1/1/3
3	DGL	A	505[B]	4	-	7/8/8/9	-
2	0JC	B	503	1	-	-	0/1/1/3
2	0JC	A	502[A]	-	-	-	0/1/1/3
2	0JC	B	506	1	-	-	0/1/1/3
2	0JC	A	502[B]	1	-	-	0/1/1/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	501[B]	6CL	OXT-C	-4.39	1.16	1.30
4	B	501[A]	6CL	OXT-C	-4.08	1.17	1.30
3	A	505[A]	DGL	CB-CG	3.12	1.63	1.53
4	B	501[B]	6CL	OH2-CZ	-2.49	1.22	1.30
4	B	501[A]	6CL	OH2-CZ	-2.37	1.23	1.30
3	A	505[B]	DGL	OXT-C	-2.09	1.24	1.30

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	501[B]	6CL	OXT-C-O	-5.04	112.65	124.08
4	B	501[A]	6CL	OXT-C-O	-4.94	112.88	124.08
4	B	501[B]	6CL	CB-CA-N	3.70	119.77	110.12
2	B	505[B]	0JC	C2-C1-N1	-3.62	93.15	108.12
4	B	501[A]	6CL	CB-CA-N	3.34	118.82	110.12
3	A	505[A]	DGL	OE1-CD-CG	-3.32	98.51	126.30
3	A	505[A]	DGL	OXT-C-O	-2.99	117.31	124.08
3	A	505[A]	DGL	CG-CB-CA	2.78	124.13	115.24
4	B	501[A]	6CL	CD-CE-NZ	2.76	117.31	110.12
3	A	505[A]	DGL	CB-CG-CD	-2.64	104.87	112.27
3	A	505[B]	DGL	OE1-CD-CG	-2.49	105.49	126.30
3	A	505[B]	DGL	OXT-C-O	-2.31	118.83	124.08
4	B	501[A]	6CL	CD-CE-CZ	2.08	115.95	110.45

There are no chirality outliers.

All (26) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	505[B]	DGL	O-C-CA-N
3	A	505[B]	DGL	N-CA-CB-CG
3	A	505[B]	DGL	C-CA-CB-CG
4	B	501[A]	6CL	N-CA-CB-CG
4	B	501[A]	6CL	C-CA-CB-CG
4	B	501[A]	6CL	O-C-CA-N
4	B	501[B]	6CL	N-CA-CB-CG
4	B	501[B]	6CL	C-CA-CB-CG
4	B	501[B]	6CL	O-C-CA-N
3	A	505[B]	DGL	OXT-C-CA-N
4	B	501[A]	6CL	OXT-C-CA-N
4	B	501[B]	6CL	OXT-C-CA-N
3	A	505[B]	DGL	CA-CB-CG-CD
4	B	501[A]	6CL	CA-CB-CG-CD

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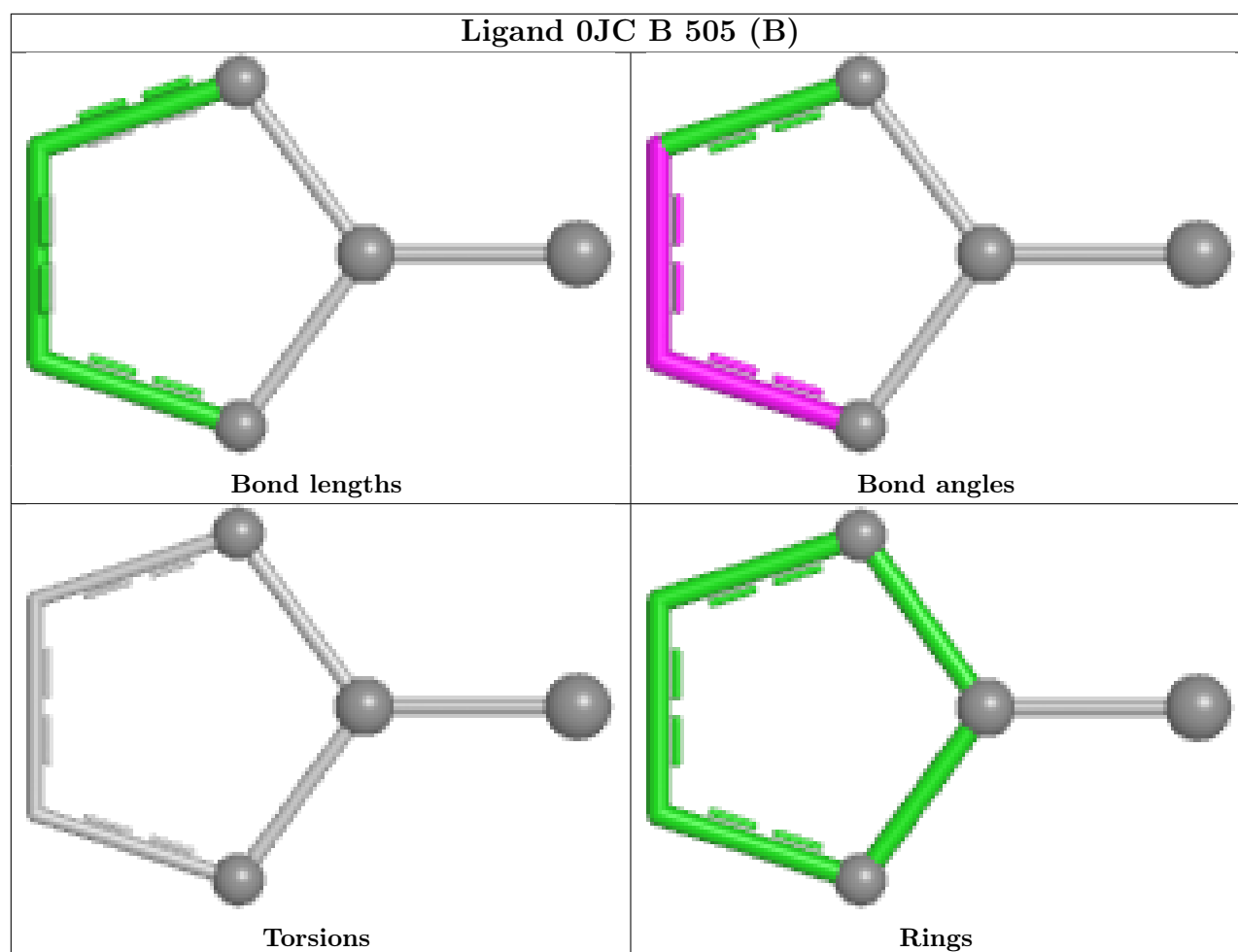
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Mol	Chain	Res	Type	Atoms
4	B	501[B]	6CL	CA-CB-CG-CD
4	B	501[A]	6CL	CE-CD-CG-CB
4	B	501[B]	6CL	CE-CD-CG-CB
4	B	501[B]	6CL	CD-CE-CZ-OH2
3	A	505[B]	DGL	OXT-C-CA-CB
4	B	501[B]	6CL	CD-CE-CZ-OH1
3	A	505[B]	DGL	O-C-CA-CB
4	B	501[A]	6CL	NZ-CE-CZ-OH2
4	B	501[A]	6CL	CD-CE-CZ-OH1
4	B	501[A]	6CL	CD-CE-CZ-OH2
3	A	505[A]	DGL	OXT-C-CA-N
4	B	501[B]	6CL	NZ-CE-CZ-OH1

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	258/408 (63%)	0.72	35 (13%)	7 7	14, 22, 41, 59	3 (1%)
1	B	269/408 (65%)	0.95	47 (17%)	4 4	12, 24, 45, 73	3 (1%)
All	All	527/816 (64%)	0.83	82 (15%)	5 5	12, 23, 44, 73	6 (1%)

All (82) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	132	GLY	14.2
1	B	131	LEU	8.2
1	B	150	HIS	7.5
1	B	122	ARG	7.0
1	B	129	THR	6.7
1	A	407	LYS	5.7
1	B	407	LYS	5.6
1	B	124	TYR	5.3
1	A	237	MET	4.6
1	A	155	TYR	4.5
1	B	123	ARG	4.3
1	A	231	VAL	4.3
1	B	402	ARG	4.1
1	B	236	GLY	4.1
1	A	244	GLN	4.0
1	A	233	LEU	4.0
1	B	230	GLY	3.7
1	B	151	LEU	3.5
1	A	246	HIS	3.4
1	B	153	MET	3.4
1	A	189	LYS	3.1
1	A	398	TRP	3.1
1	B	126	LEU	3.0
1	A	179	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	271	GLU	2.9
1	B	268	VAL	2.9
1	B	237	MET	2.9
1	A	186	LYS	2.9
1	A	238	PHE	2.8
1	B	128	ALA	2.8
1	A	173	ARG	2.8
1	B	398	TRP	2.8
1	A	157[A]	MET	2.8
1	A	308	TYR	2.8
1	A	299	LYS	2.8
1	B	238	PHE	2.8
1	A	406	ALA	2.7
1	B	173	ARG	2.7
1	B	371	ARG	2.7
1	A	235	GLU	2.7
1	A	150	HIS	2.7
1	B	130	ALA	2.7
1	A	151	LEU	2.7
1	A	177	ASN	2.6
1	B	125	THR	2.6
1	B	155	TYR	2.6
1	B	217	LYS	2.6
1	A	371	ARG	2.6
1	A	234	GLY	2.5
1	B	308	TYR	2.5
1	A	297[A]	ARG	2.5
1	A	229	TYR	2.5
1	A	399	ASP	2.5
1	B	179	ALA	2.5
1	B	186	LYS	2.5
1	A	156	VAL	2.5
1	B	198	GLY	2.5
1	B	200	PHE	2.4
1	A	178	ILE	2.4
1	B	189	LYS	2.4
1	A	196[A]	VAL	2.3
1	B	246	HIS	2.3
1	A	309	GLY	2.3
1	A	245	THR	2.3
1	B	403	ALA	2.3
1	B	241	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	399	ASP	2.3
1	B	195	PRO	2.2
1	B	157	MET	2.2
1	B	233	LEU	2.2
1	B	206	ARG	2.2
1	B	297	ARG	2.2
1	A	217	LYS	2.2
1	A	200	PHE	2.1
1	B	397	PRO	2.1
1	B	183	ALA	2.1
1	B	231	VAL	2.1
1	A	183	ALA	2.1
1	B	234	GLY	2.0
1	A	403	ALA	2.0
1	B	232	ASP	2.0
1	B	273	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

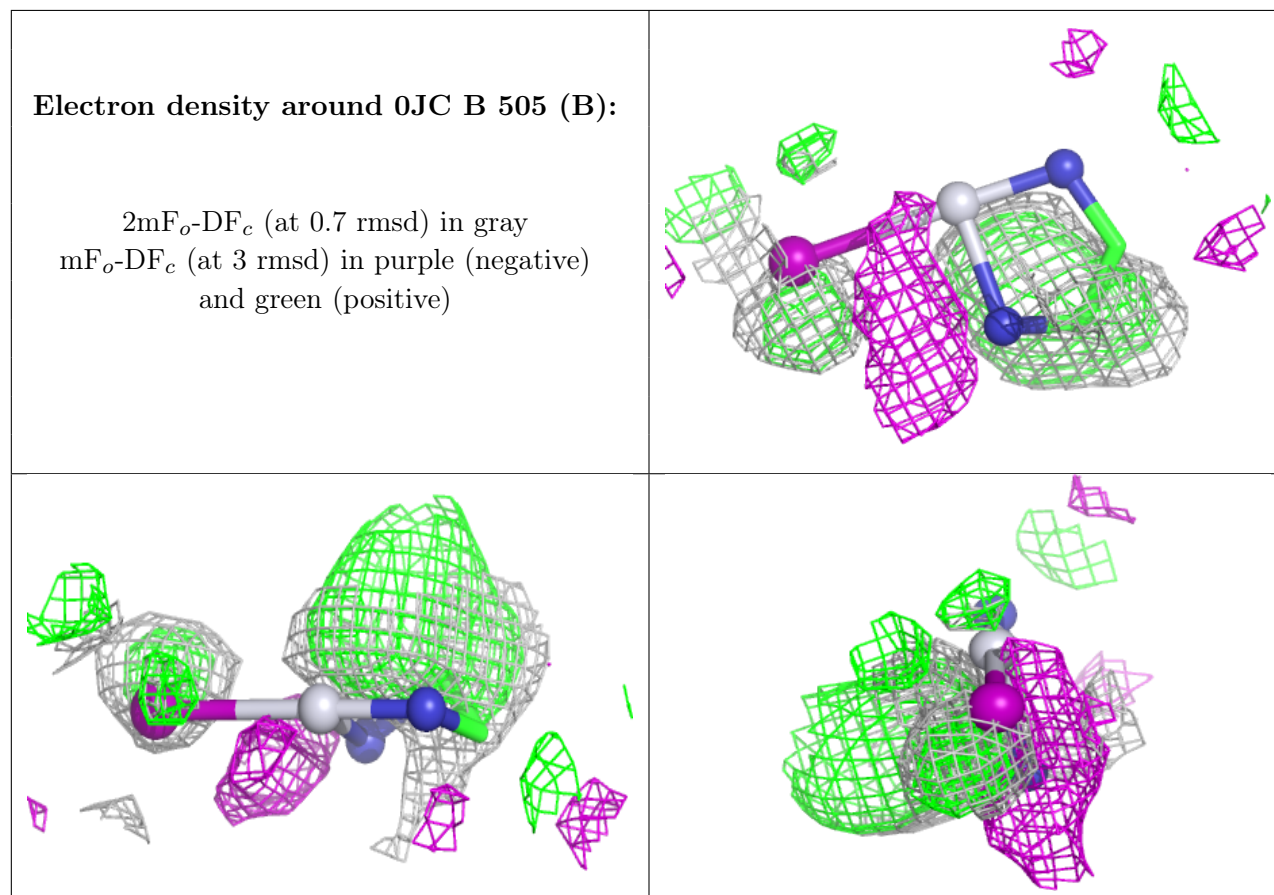
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	OJC	A	501	6/12	-	-	41,44,47,50	6
2	OJC	A	502[A]	6/12	-	-	93,94,100,106	6
2	OJC	A	502[B]	6/12	-	-	45,48,52,79	6
2	OJC	A	503	6/12	-	-	60,62,63,69	6
2	OJC	A	504[A]	6/12	-	-	86,88,100,101	6
2	OJC	A	504[B]	6/12	-	-	92,94,103,105	6
2	OJC	B	503	6/12	-	-	53,57,59,76	6

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	OJC	B	504	6/12	-	-	129,129,130,137	6
2	OJC	B	505[A]	6/12	-	-	5,25,33,36	6
2	OJC	B	505[B]	6/12	-	-	5,36,59,74	6
2	OJC	B	506	6/12	-	-	58,66,68,76	6
3	DGL	A	505[A]	9/10	-	-	37,46,48,48	9
3	DGL	A	505[B]	9/10	-	-	39,53,55,56	9
4	6CL	B	501[A]	13/13	-	-	22,31,35,36	13
4	6CL	B	501[B]	13/13	-	-	29,34,41,41	13
5	PT	B	502	1/1	-	-	73,73,73,73	1

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers ⓘ

There are no such residues in this entry.